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Comparison of the predicted amino acid sequence of the *T. aureum* probe 'TA-PKS-1-consensus' and the homologous region on ORF A of *Schizochytrium* PKS gene cluster (Accession number AAK72879).

Quality: 1269 Length: 525
Ratio: 2.469 Gaps: 10
Percent Similarity: 61.690 Percent Identity: 52.849

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

TA-PKS-1-consensus.pep x aak72879.genpept..

```
1 LCKTLDLEWPH..VFARSIDIELGANEETAAQAIFEELSCPDLTVREAGY 48
  |||: || |. | :| | . | || | | :. | | : || |
2277 LCKTIGLEWSESDVFSRGVDIAQGMHPEDA AAVIVREMACADIRIREVGI 2326

49 TKDGKRWTTEARPVGLGPKQALRSSDVLVSGGARGITPVCVRELAKSI 98
  . | | | . | |. : | | || || || || |. | : | : |
2327 GANQQRCTIRAAKLETGNPQRQIAKDDVLLVSGGARGITPLCIREITRQI 2376

99 SGGTFVLLGRSPL.ADDPAWACGV.EEANIGTAAMAHKAEFAAGRGPKP 146
  . || : || || | . | : || | : : | : | | | | | | | |
2377 AGGKYILLGRSKVSASEPAWCAGITDEKAVQKAATQELKRAFSAGEGPKP 2426

147 TPKAHKALVGSVLGAREVLGSLESIRAQGARA EYVSCDVSCAERVKAVVD 196
  ||: | | || || || || | : . | | | : | | || | . | | |
2427 TPRAVTKLVGSVLGAREVRSSIAAIEALGGKAIYSSCDVNSAADVAKAVR 2476

197 DLERRVGA.VTGVVHASGVL RDKSVERLELADFEVVYGTKVDGLLNLLQA 245
  | | .. | | . | : || || || || : : | : : | : || | | | |
2477 DAESQLGARVSGIVHASGVL RDLIEKKLPDEFDAVFGTKVTGLENLLAA 2526

246 VDRPKLRHLVLFSSLAGFHGNTGQAVYAMANEALNKMAFHLETAMPGLSV 295
  || | | : | : || || || || || | | | | | | | | | | | |
2527 VDRANLKMVLFSSLAGFHGNVQSDYAMANEALNKMKG..LELA.KDVSV 2573

296 KTIGFGPWDGGMVNDALKAHFASMGVQIIPLDGAETVSRIIGACSPTQV 345
```

FIG.1A

```

      |.| ||||| || | ||||| :||:|.||: || ::
2574 KSICFGPWDGGMVTPLKKQFQEMGVQIIPREGGADTVARIVLGSSPAEI 2623

      . . . . .
346 LVGNWGLPPVVPNASVHKITVRLGGESANPFLSSHTIQGRKVLPMTXALG 395
      |||| | . : :: .| |||| | |||:|||| |:|
2624 LVGNWRTPSKKVGSDTITLHRKISAKS.NPFLEDHVIQGRRVLPMTLAIG 2672

      . . . . .
396 LLAEAARGLYVGHQVXGIEDAQVFQGVVLDKGATCEVQLRRESSTASPSE 445
      ||| ||: |: . |:|.|.|| .| ||| | |||
2673 SLAETCLGLFPGYSLWAIDDAQLFKGVTVDGDVNCEVTL..TPSTAPSGR 2720

      . . . . .
446 VVLSASLNVFAAGKVVPAYRAHVIGASGPRTGGVQLELKDLDGVDADPAC 495
      | . |.| |..|.||||| :|| | :| |||||
2721 VNVQATLKTFSGKLVPAYRAVIVLSNQGAPPANATMQPPSL..DADPAL 2768

      . . . . .
496 SVGKGALYDGRTLFGPAFQYMDEV 520
      .|..||:|||||||. .|:|
2769 ...QGSVYDGKTLFGPAFRGIDDV 2790

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FIG.1B

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Comparison of the predicted amino acid sequence of the *T. aureum* probe
 'TA-PKS-1-consensus' and the homologous region on ORF 5 of *Shewanella* PKS
 gene cluster (Accession number AAB81123).

Quality: 641 Length: 551
 Ratio: 1,233 Gaps: 16
 Percent Similarity: 47.379 Percent Identity: 39.919

Match display thresholds for the alignment(s):

| = IDENTITY
 : = 2
 . = 1

TA--PKS-1-consensus.pep x aab81123.genpept

```

      .      .      .      .      .
1  LCKTLDLEWPHVFARSIDIELGANEETAAQAIFEELSCPDLTVREAGYTK 50
   | ||| ||| || |.:|| .   | || ||   . | | .
2094 LTKTLSHEWPQVFCRALDIATDVDATHLADAITSELFDSQAQLPEVGLSL 2143

      .      .      .      .      .
51 .DGK..RWTTEARPVGLGKPKQALRSSDVLVSGGARGITPVCVRELAKS 97
   ||| | | |   | | |. | ||. |||: |: | | | |
2144 IDGKVNRTLVAEEAADKTAKAELNSTDKILVTGGAGVTFECALALA.S 2192

      .      .      .      .      .
98 ISGGTFVLLGRSPLADDPAWACGVVEEANIGTAAMAHLKAFAAGRGPCKPT 147
   | |:| ||| | |. || | : . : . ||. ||:   | |||
2193 RSQSHFILAGRSELQALPSWAEGKQTSELKSAAIAHI.....ISTGQKPT 2237

      .      .      .      .      .
148 PKAHKALVGSVLGAREVLGSLESIRAQGARA EYVSCDVSCAERVKAVVDD 197
   || .| | | . |: . | .   || ||||| ||. . : |
2238 PKQVEAAVWPVQSSIEINAALAFNKGASAEYVSM DVTDSAAITAA... 2284

      .      .      .      .      .
198 LERRVGAVTG VVHASGVLRDKSVERLELADFEVVYGTKVDGLLNLLQAVD 247
   | | :||.:| .||| || :: ||: |||||. || || |.:
2285 LNGRSNEITGLIHGAGVLADKHIQDKTLAELAKVYGTKVNGLKALLAALE 2334

      .      .      .      .      .
248 RPKLRHLVLFSSLAGFHGNTGQAVYAMANEALNKMAFHLETAMPGLSVKT 297
   |:: | :||| |||: || ||. |||. |: ||| |   | | .
2335 PSKIKLLAMFSSAAGFYGNIGQSDYAMSNDILNKAALQFTARNPQAKVMS 2384

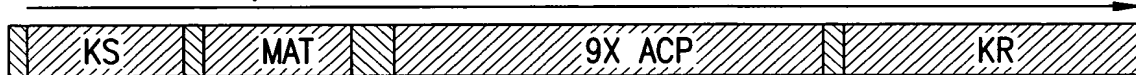
      .      .      .      .      .
298 IGFGPWDGGMVNDALKAHFASMGVQIIPLDGGAETVSRIIGACSPTQVLV 347
  
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FIG.2A

FIG. 2B

Organization of PUFA-PKS genes from *Thraustochytrium aureum* ATCC 34304

ORF A-8748 bp



ORF B-6123 bp



KS= β -keto acyl synthase
 MAT=MalonylCoA
 transferase
 ACP=Acyl carrier protein
 KR=Ketoacyl-ACP reductase
 AT=Acyl transferase

FIG.3

Sequence ID Nos. and Corresponding Sequences:

SEQ ID NO 1:

5'-AGC GGA TAA CAA TTT CAC ACA GG-3'

SEQ ID NO 2:

CACGAGGCCAAGCATTTCGAGCAAAGCGCTCAACCAGCAGATCCCAGG
 CGGGCGCGCCTGCTTCGTGGGCGTCTCGCGAATCGACGGACAGCTCG
 GACTTAGCGGAGCTTGCGCGAAAGGAAAGGGCTGGGCTGAGGCCGCA
 GAGATTGCTCAGCAAGGAGCCGTCGCAGGCTTGTGCAAGACCTTGGA
 CCTAGAGTGGCCGCACGTCTTCGTGCGCAGCATCGACATCGAGCTTGG
 CGCGAACGAAGAAACAGCTGCGCAAGCAATCTTTGAGGAGCTCTCTT
 GCCCCGACCTAACGGTGCGCGAAGCAGGATACACCAAAGACGGCAA
 GCGGTGGACGACTGAGGCGCGACCGGTTGGGCTTGGCAAGCCCAAGC
 AGGCACTACGTTCTTCGGACGTCTTCTTGGTTTCTGGTGGGGCGCGGGG
 AATTACACCTGTTTTCGTTTCGCGAGTTGGCCAAATCGATCAGTGGTGG
 CACTTTTGTCTCTCTCGGGCGGTCCCCTCTCGCTGATGATCCGGCGTGG
 GCTTTCGCGCGTCGAGGAAGCAAACATTGGGACAGCCGCTATGGCGCA
 CCTCAAGGCCGAGTTTCGCAGCCGGGCGCGGCCCGAAGCCGACGCCAA
 AGGCCACAAAGCACTCGTTGGGAGCGTCCTGGGGGCGCGCGAAGTC
 CTTGGTTCGCTAGAGAGTATTCGCGCCCAGGGTGCGCGCGCCGAGTAC
 GT

SEQ ID NO:3:

TCGCCAACACAAGTTCTGGTTGGCAACTGGGGCTTGCCCCCTGTAGTT
 CCTAACGCGAGCGTGCACAAGATTACTGTGAGGCTTGGCGGGGAGTC
 TGCAAACCCTTTCCTGTCCTCCCACACGATTCAAGGCAGAAAGGTCTT
 GCCGATGACTGYGGCGCTTGGGCTTCTCGCTGAGGCGGCTCGAGGGCT
 CTACGTCGGTACCAAGTAGYCGGGATTGAGGACGCCCAAGTCTTCCA
 GGGAGTCGTGTTGGACAAAGGGGCGACGTGTGAGGTCCAGCTTCGCC
 GCGAGTCTTCGACTGCAAGCCCAAGCGAGGTTGTGCTGAGTGCTTCGC
 TCAATGTATTTCGCGGCGGGAAAGGTTGTGCCTGCGTACCGCGCGCATG
 TCGTGCTCGGCGCTTCAGGGCCACGCACTGGCGGCGTGCAGCTTGAAC
 TGAAAGATTTGGGCGTGGACGCCGACCCTGCTTGCTCCGTTGGCAAGG
 GTGCGCTGTACGACGGTAGGACGCTGTTCCATGGGCGGCGGCTTTCAGT
 ACATGGATGAGGTTCCCTGGTGCTCGCCTGCAGAGCTTGCCGTGCGGT
 GCCGTGTCGTTCCGAGCGCGGCTCAGGACCGCGGCCAATATGTTTCGC
 GCGGAGTGTTGTACGACCCGTTCCCTGAACGACACGGTGTTTCAAGCTC
 TCCTTGTTTGGGCCCGTCTGGTTCAGGGACAGCGCTTCGCTACCGAGCA
 ACGTTGAACGAATCTCGTTCCACGGCCAGCCGCCGAGCGAGGGCGAG
 GTGTAGTACACCACGCTCAAGCTGGACAGTGCTGCGAGCGGGCCGCT
 CGACCCGATTGCAACAGGCGCATTTCTTCCCTCCACCGAGCTTGCGGGG
 CGGTCTTTGCATCAGGGCGAGCGAGTGTTGTTCTGAACAAGGCTCTTT
 CGTATGATGGCTCTCGACCCAAAGGCGAGTAGAGTACTCTACTCAGTA

FIG.4-1

CTCCTTTTCACATACCGGCAGGCAGCGTTGCTGTGGGATGGCCGGGGG
CTCTTCTGCACGCGGCTCC

SEQ ID NO:4:

GAATTCGGCACGAGGCCGGCCTCACGACGCAGGTTGTTCCGTTCCGCG
CTGCAGGTCTGTACGCAACGCGGACGGCTCTGTTTCGAGTCCGCAACC
GCATCATCGGAAAGATTTTCGCGCACGGAGCTCGCGGAGATGTTTCATTC
GCCCCGCTCCGGAGGCCCTCTTGACCAAGTTGGTTGCGTCGGGTGAGA
TTTCGGCCGAGCAGMNGCCTGGCCAAACAAGTGCCGATGCCGACGAC
ATTGCCGTCGAGSAGAACTCGGGCGGCCACACGGACAATCGCCCGAT
CCATGTTCATCCTTCCGCTGATCATCGCGCTCCGCAACAGGCTGCACAA
GGAGTGCGGTTACCCGGCGAGCCTTCGCGTTCGAGTTGGCGCGGGTGG
CGGGATCGGCTGCCCGCTTGACGCAACTGCGGCCTTCAACATGGGCGC
CGCCTTTCTCGTGACAGGAACAGTCAACCAACTCAGCCGGCAGTCGG
GCACCTGCGACGCGGTGCGCATSAGCTTTTCAAAGCGACCTACTCGG
ACATCACAATGGCGCCCCGCCGACAGATATGTTTGACCAGGGGGTTGAG
CTCCAGGTGCTCAAGAAGGGCACCATGTTTCCGTCGCGCGCCAAGAA
GCTCTACGAGCTGTTTTGCACGTACAACCTCGKTCGACGAGATGCCCCG
CGAGGAGCTCGCGCGGGTTGAGAAGCSGATYTTCCAAAAGCCCCTCG
CGGSCGTATGGGACGAGACGAAAGACTTTTACATCAACCGTCTCCACA
ACGAGGACAAGATCGAACGCGCGAGAAAAGGATGGCAAGCTCAAGAT
GTCGCTCTCGTTCCGCTGGTACCTTGGCCTGAGTTCGTTCTGGGCCAAC
AATGGAATCGCCGACCGCGTGCTGGACTATCAAGTGTGGTGCGGCCCT
GCGATTGGGGCCTGGAACGACTTTGCCAAGGGATCCTACCTCGACGCC
GAGGTCTGCGGCCAGTTTCCTTGCGTTGTGCAGGTCAACCTGCAGATC
CTCCACGCGCGGCCTACATGCAGCGCCTTCTGGCCGTCAAGCATGACC
CGCGCATCGAGTTTGACCTCGAGGACCCGGTCTTTGGTACGCCCCCAC
TGCCGCGCTCTAAAGCGATGCAGCAACGCACTCTTTCGGAGGCCCGTC
GCTGCAGCACTTGTGCGAACTCGATAGGGTTTCTTTCAAGATTTCAATC
AACAAAACAAGTATTGGAATGACAAAAAATAAAAAAACTCGAG

SEQ ID NO:5:

5'- CTT GTG CAA GAC CTT GGA CCT AGA G-3'

SEQ ID NO:6:

5'-GAA CCT CAT CCA TGT ACT GAA ACG C-3'

SEQ ID NO:7:

TTGTGCAAGA CCTTGGACCT AGAGTGGCCG CACGTCTTCG
CTCGCAGCATCGACATCGAG CTTGGCGCGA ACGAAGAAAC
AGCTGCGCAA GCAATCTTTGAGGAGCTCTC TTGCCCGGAC
CTAACGGTGC GCGAAGCAGG ATACACCAAAGACGGCAAGC
GGTGGACGAC TGAGGCGCGA CCGGTTGGGC TTGGCAAGCC
CAAGCAGGCA CTACGTTCTT CGGACGTCTT CTTGGTTTCT
GGTGGGGCGCGGGGAATTAC ACCTGTTTGC GTTCGCGAGT

FIG.4-2

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TGGCCAAATC GATCAGTGGTGGCACTTTTG TCCTCCTCGG
GCGGTCCCCT CTCGCTGATG ATCCGGCGTGGGCTTGCGGC
GTCGAGGAAG CAAACATTGG GACAGCCGCT ATGGCGCAC
TCAAGGCCGA GTTCGCAGCC GGGCGCGGCC CGAAGCCGAC
GCCAAAGGCCACAAAGCAC TCGTTGGGAG CGTCCTGGGG
GCGCGCGAAG TCCTTGGTTCGCTAGAGAGT ATTCGCGCCC
AGGGTGC GCG CGCCGAGTAC GTTTCCTGCGACGTTTCGTG
TGCGGAGCGC GTCAAGGCCG TCGTCGACGA TCTCGAGCGA
CGGGTCGGGG CTGTAAGTGG GGTGTGCAC GCCTCTGGTG
TTCTCCGAGACAAGTCCGTT GAGCGCTTGG AGCTCGCCGA
CTTCGAGGTC GTGTACGGCACCAAGGTGGA CGGCCTGCTC
AACCTGCTGC AGGCCGTGGA CCGCCCCAAACTCCGGCACT
TGGTCCTCTT CAGCTCCCTG GCCGGTTTCC ACGGCAACAC
TGGGCAGGCC GTGTACGCTA TGGCGAATGA GGCGCTGAAC
AAGATGGCCTTCCATTTGGA AACTGCGATG CCTGGCCTCT
CGGTCAAGAC GATCGGGTTTGGACCTTGGG ACGGCGGCAT
GGTCAACGAT GCGCTGAAAG CGCACTTTGCGTCTATGGGC
GTCCAAATTA TTCCGCTCGA CGGYGGCGCG GAGACCGTTT
CCCGAATCAT CGGGGCGTGC TCGCCAACAC AAGTTCTGGT
TGGCAACTGGGGCTTGCCCC CTGTAGTTCC TAACGCGAGC
GTGCACAAGA TTAAGTGAGGCTTGGCGGG GAGTCTGCAA
ACCCTTTTCTT GTCCTCCAC ACGATTCAAGGCAGAAAGGT
CTTGCCGATG ACTGYGGCGC TTGGGCTTCT CGCTGAGGCG
GCTCGAGGGC TCTACGTCGG TCACCAAGTA GYCGGGATTG
AGGACGCCCAAGTCTTCCAG GGAGTCGTGT TGGACAAAGG
GGCGACGTGT GAGGTCCAGCTTCGCCGCGA GTCTTCGACT
GCAAGCCCAA GCGAGGTTGT GCTGAGTGCTTCGCTCAATG
TATTCGCGGC GGGAAAGGTT GTGCCTGCGT ACCGCGCGCA
TGTCGTGCTC GGCGCTTCAAG GGCACGCAC TGGCGGCGTG
CAGCTTGAAGTGAAGATTT GGGCGTGGAC GCCGACCCTG
CTTGCTCCGT TGGCAAGGGTGCGCTGTACG ACGGTAGGAC
GCTGTTCCAT GGGCCGGCGT TTCAGTACATGGATGAGGTT C

SEQ ID NO:8:

CGCAAGTGCATCCGGCCATCATTGGGCCATCATTGGGCCATCATTGGT
GTTTTGGGCGCGCTTTGCGGATCGTCCGGCCGATCAGGTACGAGGCC
ACGAACCTACGTCGTTTGCCGCGCTCAGGCTGGTTGGTTGCACTTGA
CTCTTCTGTGACCTTTCATCGTGTGCAGGCAAACGCAAGTGGAGTGCGTCG
GAGACACGGCGAAGGATCCGTGCTGCAAACGCAAGTGGAGTGCGTCG
AGAGCACCGCCGAGACCAAGAGCCGAGGCAGACAAGGCCAGCAACG
AGATGGAGACAAAGGACGATCGCGTTGCGATCGTGGGCATGTCGGCC
ATACTGCCTTGCGGTGAGTCAGTGCGCGAGTCGTGGGAGGCGATTGCG
GAGGGGCTCGATTGCCTGCAGGACCTGCCTGCGGACCGAGTCGATAT
CACGGCGTACTACGACCCGAACAAGACAACCAAGGACAAGATCTACT
GCAAGCGCGGCGGCTTCATTCGAGTATGACTTTGACGCGCGCGAGT

FIG.4-3

TCGGCCTCAACATGTTCCAGATGGAGGACTCGGACGCCAACCAAACC
 GTGACTTTGCTCAAGGTCAAGGAGGCTCTCGAGGACGCCGGGGTGGGA
 GCCCTTCACAAAGAAGAAGAAGAACATTGGCTGCGTGCTCGGCATCG
 GCGGCGGGCAGAAAGGCGAGCCACGAGTTTTACTCCCGACTCAACTAT
 GTGGTCGTGGAGAAGGTGCTTCGCAAGATGAACCTCCCCGACGAGGT
 TGTCGAGGCCGCGTCGAAAAGTACAAGGCCAACTTTCCTGAATGGC
 GCCTCGACTCGTTCCCTGGGTTTCTTGGAACGTGACCGCCGGGCGGT
 GCAGCAACGTCTTCAACATGGAAGGCATGAACTGCGTCGTGGACGCT
 GCGTGCGCCAGCTCGCTCATCGCGATCAAGGTTGCCATTGATGAGCTC
 CTCCACGGGGACTGCGACACCATGATTGCCGGTGCGACCTGCACCGA
 CAACTCGATCGGGATGTACATGGCCTTTTCCAAAACCCAGTTTTCTCC
 ACCGACCAGAGCGTCAAGGCGTACGACGCCAAGACGAAAGGCATGC
 TCATCGGCGAAGGCTCGGCCATGGTCGTGCTCAAGCGGTACGCGGAC
 GCCGTTTCGGGATGGTGATGAGATCCATGCCGTCATCAGGGCATGCGCC
 TCGTCCAGCGACGGCAAGGCTGCTGGCATTACGCACCGACGGTGTCG
 GGTCAAGAAGAGGCACTGCGGCGCGCGTACGCCCCGAGCTGGCGTGGA
 CCCCTCCACCGTCACGCTGGTGAGGGGCCACGGCACTGGCACACCCG
 TCGGGGACCGGATTGAGCTGACCGCCTTGCGCAACGTCTTTGACGCAG
 CCAACAAAGGCCGCAAGGAAACAGTCGCGGTGGGAAGCATCAAGTC
 GCAGATCGGTACCTGAAGGCCGTGGCCGGCTTTGCCGGTCTCGTCAA
 GGTTGTCATGGCCCTCAAGCACAAAGACGCTGCCGCAGACCATCAACG
 TTCACGACCCGCCCCGCACTGCACGACGGCTCGCCCATCCAGGATTCTGA
 GTCTTTACATCAACACGATGAACCGGCCCTGGTTTACGGCACCTGGCG
 TCCCCCGCCGTGCAGGCATCTCTAGCTTTGGGTTTGGCGGCGCCAACT
 ACCACGCTGTTCTCGAAGAGGCCGAGCCTGAGCACGCGAAGCCGTAT
 CGCATGAACCAAGTTCCAACAACCGGTGCTCTTGACGCAAGCTCCGCG
 TCAGCTCTTGCCTCCATCTGCGACGCTCAGGCCGACGCGCTCCAGGCC
 GCCGTCTCGCCCCGAAGCCAGCAAGCACGCAAGTACCGCGCCATCGT
 AGCGTTCCATGAAGCGTTTAAGCTTCGCGCTGGAGTGCCGGGCCGGCCA
 TGCTCGAATTGGCTTTGTGTCCGGCAGCGCGGCAGCAACGCTTGCACT
 GCTCCGAGCCGCCTCTGCAAACTCAAGCAGTCGAGTGCGACGCTCG
 AATGGACCCTGCTCCGCGAGGGCGTCACGTACCGCTCCGCCGCGATG
 CAACTCCTGGCAGTGTCGCTGCTCTGTTTGCCGGGCAAGGCGCGCAG
 TACACGCACATGTTTCGCTGACGTTGCCATGAACTGGCCACCGTTTCTGA
 AGCGCCGTGCAAGAGATGGATGCCGCTCAAGTCACGGCGGCAGCGCC
 GAAGCGCCTCAGCGAGGTCCTGTATCCGCGCAAGCCGTACGCTGCAG
 AGCCCGAGCAAGACAACAAGGCCATCTCGATGACGATTAACCTCGCAA
 CCGGCCCTCATGGCCTGCGCTGCTGGGGCGTTTGAGGTGTTTCGTCAA
 GCTGGTCTTGCGCCCCGACCACGTGCGGGTCATTCTCTCGGCGAGTTT
 GGTGCTTTGCTCGCCGCTGGATGCGCAAGCCGTGAGGAGCTCTTCCGT
 CTGGTCTGCAGCAGAGCGAAGGCAATGCAAGACGTTCCCAAGCCAAG
 CGAGGGCGTCATGGCAGCTGTCATCGGCCGTGGTGCTGACAAGCTCA
 CGCTGCAAGGCGATGGTGCGTGGCTTGCCAACTGCAACTCGCCAAGC
 CAAGTGGTCATTTCCGGCGACAAGACTGCTGTCGAGCGTGAATCCAGC
 CGGTTGGCAGGCCTTGCTTCAGGATCATTCCGCTTGCAATGCGAAGGC

FIG.4-4

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GCCTTCCATTACCGCACATGACGGCGGCCAGGCCACGTTTCAGGCT
GCACTGGACAGCCTCAAGATCTCCACCCCGACGAACGGGGGCGGCCT
GTACAACAACGTTTCCGGAAAGACCTGCCGATCCCTGGGTGAACTCC
GCGACTGCCTGGGCAAGCACATGACAAGTCCTGTGCTCTTCCAGGCAC
AGGTAGAGAACATGTACGCTGCCGGGGCGCGCATTTTCGTGGAGTTTG
GCCCCGAAGCAAGTCCTCTCCAAGCTCGTAGGCGAGATTCTCGCCGAC
AAGTCAGACTTTGTGACAGTCGCGGTCAACTCGTCATCGTCCAAGGAC
AGCGACGTGCAACTTCGTGAAGCTGCTGCGAAGCTCGCGGTCTTTGGC
GTCCCGTTGGCGAACTTTGACCCTTGGGAGCTCTGCGACGCGCGGCGT
CTTCGCGAATGCCCGCGATCCAAGACGACGTTGCGCTTGTCTGCAGCG
ACCTACGTGTGCAACAAGACCCTTGCTGCTAGGGAGAAGGTCATGGA
GGACA ACTGCGACTTTTCTTCGCTCTTTGCCTCCGGTCCAGCAAGCCA
AGAGATGGAGCGAGAAATAGCCAACCTTCGCGCTGAGCTGGAGGCGG
CCCAACGCCAGCTTGACACGGCCAAAACCCAGCTTGCTCGAAAGCAA
GTGCAGGACCCACCGCTGACCGACAGCGCGATATGATTGCCAAGCA
CCGATCCACACTCGCAGCAATGGTGAAGGAATTCGAGGCTCTGGCAA
GTGGTAGTCCTTGCGCTGTTCCGTTTGCGCCTGTGGTGGACACTGCTGT
CGAAGACGTGCCTTTTGCGGACAAGGTCTCGACGCCACCGCCCCAAG
TCACTTCCGCTCCCATCGCCGAGCTCGCGCGCGCCGAGGCCGTCTCA
TGGAGGTTCTCGCTGCCAAGACTGGCTACGAGGTCGACATGATCGAG
GCCGACATGCTGCTCGACGCCGAGCTCGGCATCGACTCGGTCAAGCG
CATTGAGATCCTGGCAGCTGTCCAGGCCCAGCTCGGGGTCGAGGCCA
AGGACGTCGACGCGCTCAGCCGCACACGAACAGTTGGCGAGGTCGTT
GACGCCATGAAGGCTGAGATCGGCGGGCAAGCGACCAGTGCGCCTTC
GCCGATGGCCCAGCCCCAAGCCTCAGCACCATCACCGTCCCCTACTGC
CTCTGTGCTGCCTAAGCCTGTTGCTTTACCAGCTAGTGTGATCCCGCC
AAGCTCGCGCGCGCCGAAGCGGTCTCATGGAGGTTCTCGCCGCCAA
GACTGGCTACGAGGTCGACATGATCGAGGCTGACATGCTGCTCGACG
CCGAGCTCGGCATCGACTCGGTCAAGCGCATTGAGATCCTGGCGGCTG
TCCAAGCTCAGCTCGGGGTCGAGGCCAAGGATGTGACGCGCTCAGC
CGCACACGCACTGTTGGCGAGGTCGTTGATGCCATGAAGGCTGAGAT
CGGCGGGCAAGCGACCAGCGCACCTGCGTCCGTGGCCCAGCCCCAAG
CCTCAGCACCATCACCGTCCGCAACA ACTGCCTCTGTGCTGCCTAAGC
CTGTTGCTGCACCAACTAGCGCCGATCCCGCCAAGCTCGCGCGCGCCG
AAGCCGTCGTCATGGAGGTTCTCGCTGCCAAGACTGGCTACGAGGTCG
ACATGATCGAGGCTGACATGCTGCTCGACGCCGAGCTCGGCATCGACT
CGGTCAAGCGCATTGAGATCCTGGCGGCTGTCCAAGCCCAGCTCGGG
GTCGAGGCCAAGGACGTCGACGCGCTCAGCCGCACACGCACGGTTGG
CGAGGTCGTCGAGGCCATGAAGGCTGAGATCGGCGGGCAAGCGACC
AGTGCACCTGCGTCCGTGGCCCAGCCCCAAATCTCTGTGTCCCCTACG
CCTCTCGCTGCATCTCCTAGTGCCGATCCTGCCAAGCTCGCGCGCGCC
GAAGCCGTCGTCATGGAGGTTCTCGCTGCCAAGACTGGCTACGAGGTC
GACATGATCGAGGCTGACATGCTGCTCGACGCCGAGCTCGGCATCGA
CTCCGTCAAGCGCATCGAGATCCTGGCGGCTGTCCAGGCCCAGCTCGG
GGTCGAGGCCAAGGACGTCGACGCGCTCAGCCGCACACGCACTGTTG

FIG.4-5

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GCGAGGTCGTTGACGCCATGAAGGCTGAGATCGGCGGGCAAGCGACC
AGTGCGCCTGCATCCGTGGCCCAGCCCCAAGCCTCAGCACCGTCGCC
GTCCGCTACTGCCTCTGTGCTGCCTAAGCCTGTTGCTGCACCAACTAGC
GCCGATCCCGCCAAGCTCGCGCGCGCCGAAGCCGTCGTCATGGAGGT
TCTCGCTGCCAAGACTGGCTACGAGGTCGACATGATCGAGGCTGACAT
GCTGCTCGACGCCGAGCTCGGCATCGACTCGGTCAAGCGCATCGAGA
TCCTGGCGGCTGTCCAAGCCCAGCTCGGGGTCGAGGCCAAGGACGTC
GACGCGCTCAGCCGCACACGCACGGTTGGCGAGGTCGTCGAGGCCAT
GAAGGCTGAGATCGGCGGGCAAGCGACCAGTGACCTGCGTCCATGG
CCCAGCCCCAAATCTCTGTGTCCCCTACGCCTCTCGCTGCATCTCCTAG
TGCCGATCCTGCCAAGCTCGCGCGCGCCGAGGCCGTCGTCATGGAGGT
TCTCGCTGCCAAGACTGGCTACGAGGTCGACATGATCGAGGCCGACA
TGCTGCTCGACGCCGAGCTCGGCATCGACTCGGTCAAGCGCATCGAG
ATCCTGGCGGCTGTCCAAGCTCAGCTCGGGGTCGAGGCCAAGGACGT
CGACGCGCTCAGCCGCACACGCACGGTTGGCGAGGTCGTTGATGCCA
TGAAGGCTGAGATCGGCGGGCAAGCGACCAGTGCGCCTGCATCCGTG
GCCAGCCCCAAGCCTCAGCACCGTCGCCGTCCGCTACTGCCTCTGCG
CCTGTTACGCCTCTCGCTGCACCAGCTAGTGTGATCCCGCCAAGCTC
GCGCGCGCCGAAGCCGTCGTCATGGAGGTTCTCGCCGCCAAGACTGG
CTACGAGGTCGACATGATCGAGGCTGACATGCTGCTCGACGCCGAGC
TCGGCATCGACTCCGTCAAGCGGATTGAGATCCTGGCGGCTGTCCAAG
CCCAGCTCGGGGTCGAGGCCAAGGACGTGACGCGCTCAGCCGCACA
CGCACTGTTGGCGAGGTCGTTGACGCCATGAAGGCTGAGATCGGCGG
GCAAGCGACCAGCGCACCTGCGTCCGTGGCCCAGCCCCAAGCCTCAG
CACCGTCGCCGTCCGCTACTGCCTCTGTGCTGCCTAAGCCTGTTGCTTC
ACCAGCTAGTGTGATCCCGCCAAGCTCGCGCGCGCCGAAGCGGTCTG
TCATGGAGGTTCTCGCTGCCAAGACTGGCTACGAGGTCGACATGATCG
ACGCTGACATGCTGCTCGACGCCGAGCTCGGCATCGACTCCGTCAAGC
GCATCGAGATCCTGGCGGCTGTCCAAGCCCAGCTCGGGGTCGAGGCC
AAGGACGTGACGCGCTCAGCCGCACACGAACGGTTGGCGAGGTCGT
CGAGGCCATGAAGGCTGAGATCGGGGCAGCAGGTCCAAACGATGCA
CAAGCAGCGTCTGGGCATCTCTTTGGCACGGGATGTGAAGACCTGAG
CCTTTGCTCTGCTTCTGTGGTTGAGATTGCTCGTTGCAGCGAACTAGCT
CTGGAGCGCCCGATGGATCGGCCCATTCTTATTGTAAGCGATGGATCA
GCATTGCCGGCGGCTCTGGCTAGTCGACTGGGGTCGTGTGCAGTAATC
CTCACGACCGCAGGCGAGACCGACCAATCTGTGCGCTCGACGAAGCA
CGTTGACATGGAAGGGTGGGGCGAGGCAGATCTCGTGCGCGCTCTTG
AAGCAGTAGAGTCTCGATTCCGGCGTCCCAGGCGGCGTCGTGGTGCTTG
AGCGCGCCTCAGAAACAGCTAGGGACCAGCTTGGCTTTGCCCTGCTGC
TTGCCAAGCATTCGAGCAAAGCGCTCAACCAGCAGATCCCAGGCGGG
CGCGCCTGCTTCGTGGGCGTCTCGCGAATCGACGGAAAGCTCGGACTT
AGCGGAGCTTGCGCGAAAGGAAAGGGCTGGGCTGAGGCCGCAGAGA
TTGCTCAGCAAGGAGCCGTGCGGGGCTTGTGCAAGACCTTGGACCTAG
AGTGGCCGCACGTCTTCGCTCGCAGCATCGACATCGAGCTTGGCGCGA
ACGAAGAAACAGCTGCGCAAGCAATCTTTGAGGAGCTCTCTTGCCCG

FIG.4-6

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GACCTAACGGTGC GCGAAGCAGGATACACCAAAGACGGCAAGCGGT
GGACGACTGAGGCGCGACCGGTTGGGCTTGGCAAGCCCAAGCAGGCA
CTACGTTCTTCGGACGTCTTCTTGGTTTCTGGTGGGGCGCGGGGAATTA
CACCTGTTTTCGTTTCGCGAGTTGGCCAAATCGATCAGTGGTGGCACTTT
TGTCCTCCTCGGGCGGTCCCCTCTCGCTGATGATCCGGCGTGGGCTTGC
GGCGTCGAGGAAGCAAACATTGGGACAGCCGCTATGGCGCACCTCAA
GGCCGAGTTCGCGAGCCGGGCGCGGCCCGAAGCCGACGCCAAAGGCC
CACAAAGCACTCGTTGGGAGCGTCCTGGGGGCGCGCGAAGTCCTTGG
TTCGCTAGAGAGTATTCGCGCCCAGGGTGC GCGCGCCGAGTACGTTTC
CTGCGACGTTTCGTGTGCGGAGCGCGTCAAGGCCGTCGTCGACGATCT
CGAGCGACGGGTCGGGGCTGTA ACTGGGGTTGTGCACGCCTCTGGTGT
TCTCCGAGACAAGTCCGTTGAGCGCTTGGAGCTCGCCGACTTCGAGGT
CGTGTACGGCACCAAGGTGGACGGCCTGCTCAACCTGCTGCAGGCCG
TGGACCGCCCCAACTCCGGCACTTGGTCCTCTTCAGCTCCCTGGCCG
GTTTCCACGGCAACACTGGGCAGGCCGTGTACGCTATGGCGAATGAG
GCGCTGAACAAGATGGCCTTCCATTTGGAAACTGCGATGCCTGGCCTC
TCGGTCAAGACGATCGGGTTTGGACCTTGGGACGGCGGCATGGTCAA
CGATGCGCTGAAAGCGCACTTTGCGTCTATGGGCGTCCAAATTATTCC
GCTCGACGGCGGCGCGGAGACCGTTTCCCCGAATCATCGGGGCGTGCT
CGCCAACACAAGTTCTGGTTGGCAACTGGGGCTTGCCCCCTGTAGTTC
CTAACGCGAGCGTGCACAAGATTACTGTGAGGCTTGGCGGGGAGTCT
GCAAACCTTTCTGTCTCGCACACGATTCAAGGCAGAAAGGTCTTG
CCGATGACTGTGGCGCTTGGGCTTCTCGCTGAGGCGGCTCGAGGGCTC
TACGTCGGTCACCAAGTAGTCGGGATTGAGGACGCCCAAGTCTTCCAG
GGAGTCGTGTTGGACAAAGGGGCGACGTGTGAGGTCCAGCTTCGCCG
CGAGTCTTCGACTGCAAGCCCAAGCGAGGTTGTGCTGAGTGCTTCGCT
CAATGTATTCGCGGGCGGGAAAGGTTGTGCCTGCGTACCGCGCGCATGT
CGTGCTCGGCGCTTCAGGGCCACGCACTGGCGGCGTGCAGCTTGA ACT
GAAAGATTTGGGCGTGGACGCCGACCCTGCTTGCTCCGTTGGCAAGGG
TGCGCTGTACGACGGTAGGACGCTGTTCCATGGGCGGCGGTTTCAGTA
CATGGATGAGGTTCTCGGTGCTCGCCTGCAGAGCTTGCCGTGCGGTG
CCGTGTCTGTTCCGAGCGCGGCTCAGGACCGCGGCCAATTTGTTTCGCG
CGGAGTGTTGTACGACCCGTTCTGAACGACACGGTGTTTCAAGCTCT
CCTTGTTGGGCCCGTCTGGTCAGGGACAGCGCTTCGCTACCGAGCAA
CGTTGAACGAATCTCGTTCCACGGCCAGCCGCCGAGCGAGGGGCGAGG
TGTTTTACACCACGCTCAAGCTGGACAGTGCTGCGAGCGGGCCGCTCG
ACCCGATTGCAAAGGCGCAGTTCTTCTCCACCGAGCTTGCGGGGCGG
TCTTTGCATCAGGGCGAGCGAGTGTGGTTCTGAACAAGGCTCTTTCGTT
TTGA

SEQ ID NO:9:

CAAGCAATCGGCCATCGAGCTGCGCGTTGGAGCTGCCGATCGAAATC
GAAAGCAAGAGGCCACAAGGCTCAGAAAGAGATGAACCAGGGCGGG
AGAAATGACGAGGGCGTCTCGGTGGCGCGCGCGGACCCATGCCCTGA
CACGCGGATCGCTGTCGTGGGCATGGCGGTCGAGTATGCAGGGTGCC

FIG.4-7

GCGGCAAGGAAGCGTTCTGGGACACGCTCATGAACGGCAAAATCAAC
TCTGCCTGTATCTCAGACGATCGCCTCGGGTCAGCACGACGAGAAGA
GCACTATGCGCCCCGAGAGGTCAAAGTACGCCGATACGTTCTGCAACG
AGAGGTACGGATGCATCGATCCCAAAGTCGACAACGAGCACGACCTG
CTCCTCGGCCTCGCCGCGGCTGCGCTTCAAGACGCGCAGGACAGGCG
CAGCGACGGCGGCAAGTTCGACCCAGCGCAGCTCAAGCGCTGCGGCA
TTGTCAGCGGCTGCCTGTCCTTCCCGATGGACAACCTGCAAGGCGAGC
TGCTCAACCTTTACCAAGCCCATGCTGAGAGGCGGATTGGCAAGCATT
GCTTCGCGGACCAAACGCCCTGGTTCGACGCGAACCAGAGCGCTTCAC
CCGCTGCCCCGGGGACCCGAGGACCCACCGCGACCCAGCCTCCTTCGT
CGCCGGACAGCTCGGCCTCGGCCCGCTGCACTACTCGCTCGACGCCGC
CTGCGCCTCGGCCCTTTACGTTCTGCGACTCGCTCAGGACCACCTCCTC
TCGGGCGAGGCTGACTTGATGCTGTGCGGAGCGACGTGCTTCCCAGAG
CCCTTCTTCATCCTGACTGGGTTTAGCACGTTCCACGCGATGCCAGTCG
GTGAGAACGGTGTCTCGATGCCGTTTCATCGGGACACGCAAGGGCTG
ACGCCCGGCGAGGGCGGCTCGGTGATGGTGCTCAAGCGCCTCGCGGA
CGCCGAGCGCGACGGAGACCACATCTACGGGACGCTTCTTGAGGCCA
GCTTGAGCAACGCAGGCTGCGGGCTTCTCTCAAGCCGCACCAGCCA
AGCGAGGAGGCCTGCTTGAAAGCCACCTACGAGCTCGTCGGCGTGCC
GCCCCGAGACGTCCAGTACGTTCGAGTGCCACGCCACCGGCACGCCGC
AGGGCGACACCGTCGAGCTCCAAGCCGTCAAAGCCTGCTTTGAGGGC
GCAAGCCCCCGGATCGGGTCCACGAAAGGCAACTTCGGACACACCCT
CGTCGCGGCGGGCTTTGCGGGAATGTGCAAGGTTCTCCTTGCAATGGA
GCGCGGCGTGATCCCCCGACCCCGGGCGTTGACTCTGGCACCCAGAT
TGATCCCCTCGTCGTACAGCGGCGCTCCCGTGGCCGGATACGCGCGG
CGGGCCGAAACGCGCAGGACTCTCCGCATTTCGGATTCTGGGGGCACAA
ACGCGCACGCCGTCTTTGAGGAGCATATTCCCTCGAGAGCTCCGCCCG
CAGTACTCTGCCAGCCTCGCCTCGGCAGCGGACCAAACCGAAAGCTT
GCTATCGTCGGCATGGATGCCACGTTTGGATCCTTGAAGGGTCTCTCC
GCACTAGAAGCTGCGCTTTACGAGGCAAGGCACGCTGCGCGGGCCCCT
GCCTGCGAAGCGCTGGCGCTTCTTGGGCGGGGACGAGTCCTTTCTCCA
CGAGATCGGACTCGAGTGCTCTCCGCACGGGTGCTACATTGAGGACGT
GGATGTGGACTTTAAGCGACTCCGCACGCCAATGGTGCCGGAGGACT
TGCTCCGGCCGCAACAGCTCCTGGCCGTGTGACGATTGACAAGGCC
ATCCTCGACTCGGGCTTGGCCAAGGGCGGCAACGTGGCTGTCCTTGTC
GGCCTCGGGACGGACCTCGAGCTCTACCGCCACCGAGCTCGGGTTGC
GCTTAAGGAGCGTCTTCAAGGACTGGTTCGCTCTGCCGAGGGAGGAG
CCCTGACGTCTCGCCTGATGAACTATATCAATGATAGCGGAACGTCGA
CCTCCTACACGTCTGATATATCGGCAACCTCGTCGCCACGCGCGTCTCGT
CCAGTGCGGGCTTCACTGGGCCGTCGTTACCGGTCACGGAAGGGGCC
AACTCGGTCCATCGGTGCGCCCAGCTCGCCAAGTACATGCTCGACCGC
GGCGAGGTTCGACGCCGTCGTGGTTGCAGGAGTCGACCTGTGCGGGAG
CGCCGAGGCGTTCTTCGTGAGGTGCGGCCGCATGCAGATCTCGAAAA
GTCAGCGCCCCGGCCGCGCCGTTTGACCGCGCCGCAGACGGCTTCTTCG
CGGGGGAAGGGTGCGGCGCCCTCGTCTTCAAACGCCTGACTGACTGT

FIG.4-8

GTGTCTGGCGAGCGAATCTACGCGTCCCTCGACTCGGTCGTCGTCGCA
 ACCACGCCGCGCGCCGCTCTTCGTGCTGCCGCAGGGTCGGCGCGGGTT
 GACCCAGCCAGCATCGACATGGTCGAGCTGAGCGCAGATTCCCACCG
 GTTTGTGCGGGCGCCAGGCACCGTGGCTCAGCCTCTGACAGCCGAAGT
 CGAGGTCGGGGCGGTGCGGGAAGTGATCGGGACCGCGGGGAGGGGC
 TCTCGAAGCGTGGCCGTCGGATCGGTCCGCGCCAACGTCGGGGACGC
 AGGGTTTGCTTCCGGGGCCGCTGCCCTCGTAAAACTGCGCTCTGCTT
 GCACAACCGCTACTTGCGGGCTACCCAGGCTGGGATGCGCCTGCTGC
 CGGCGTGGAATTTTGGTGCCGAGCTGTACGTTTGCCGCGAGTCGCGTGC
 TTGGGTCAAGAACGCCGGCGTTGCACGGCACGCCGCAATTTCTGGCGT
 GGACGAAGGCGGGTCGTGCTATGGGCTGGTTCTTTCGGACGTGCCTGG
 GCAGTACGAGACCGGCAACCGCATCTCCCTCCAGGCCGAGTCGCCCA
 AGCTCTTGCTCCTCTCGGCTCCAGACCACGCCGCTTGCTGGACAAGG
 TGGCGGCCGAGCTCGCAGCCCTTGAGCAAGCCGACGGCTTGAGCGCC
 GCCGCGGCTGCCGTAGACCGCTTACTCGGCGAGTCGCTCGTCGGTTGC
 GCGGCTGGCAGCGGCGGGCTGACCCTTTGCTTGGTGGCTTCGCCTGCC
 AGCCTCCACAAGGAGCTTGCGCTGGCCCATCGAGGGATCCCGCGCTG
 CATCAAAGCACGGCGCGACTGGGCCAGCCCGGCAGGGAGCTACTTCG
 CCCCAGAGCCGATCGCAAGCGACCGCGTCGCGTTCATGTACGGGGAA
 GGACGAAGCCCGTACTGCGGCGTCGGCCGCGACCTCCACCGGATCTG
 GCCCGCGCTGCATGAGCGGGTGAACGCCAAGACTGTCAACCTCTGGG
 GTGACGGTGACGCCTGGCTGCTGCCACGTGCAACCTCGGCCGAGGAA
 GAGGAGCAACTCTGCCGCAACTTCGACTCGAACCAGGTTGAGATGTTT
 CGAACGGGCGTGATACATCTCGATGTGCTTGACCGACCTCGCTCGAAGC
 TTGATTGGACTGGGCCCTAAGGCGAGCTTTGGGCTCAGCCTAGGCGAG
 GTTTCATGCTCTTCGCTCTGAGCGAGTCCAAGTGTAGACTGTGCGAG
 GAAATGACCCGCAGGCTCCGTGCGTCCCCGGTGTGGAAGTTCGGAGCT
 CGCCGTGAGTTCAACGCCCTTCGAAAGTTGTGGGGGGTTCGCGCCGGG
 GGCACCCGTCGACTCGTTCTGGCAAGGTTATGTGCTGCGCGCAACGCG
 GGCTCAGGTGGAGCAAGCCATTGGGGAGGACAATCAGTTTGTGCGTC
 TCCTGATCGTGAACGACTCGCAATCAGTCCTGATCGCCGGCAAGCCGG
 CGGCGTGCGAAGCCGTAATTGCTCGCATCGGGTCTATTCTTCCCCCGCT
 GCAAGTGTGCGAAGGCATGGTGGGGCACTGTGCCGAGGTCTTGCCGT
 ACACGAGCGAGATCGGGCGCATCCACAACATGCTTCGCTTCCCATCGC
 AGGACGAAACGGGCGGTTGCAAAATGTACTCTAGCGTCTCAAAGTTCG
 CGCATCGGGCCAGTCGAGGAGAGCCAGATGGGCCCAGGCACTGAGCT
 CGTTTTCTCGCCGTCAATGGAAGACTTTGTGCGCCAGCTGTACTCGCGA
 GTTGACAGACTTTCCGGCGATCACCGAGGCGGTTTACCAGCAGGGTCAT
 GACGTGTTTGTGCAAGTGGGGCCGGACCATTCACGGTCGGCTGCTGTC
 CGCTCCACGCTTGGAACCACTCGGCGACACATCGCTGTGGCGATGGAC
 CGCAAGGGTGAGTCAGCTTGGTCGCAGCTTCTGAAAATGCTGGCTACG
 CTTGCGTCGCACCGCGTGCCGGGCGCTGGACCTTTCATCCATGTACCAC
 CCCGCAGTGGTGGAGCGTTGCAGGCTGGCGCTGGCAGCACAACGATC
 GGGCCAGCCAGAGCAGCGGAACAAGTTTTTGCACGATAGAGGTGA
 ATGGGTTCTACGACCCGGCCGACGCGACCATCCCTGAGGCCGTCGCA

FIG.4-9

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ACAATTCTGCCGGCAACTGCTGCGATTTCGCCTCCAAAGCTTGGCGCT
CCGCACGACTCGCAACCCGAGGCGGAGGCTCGCCCCGTGGGCGAGGC
CTCTGTGCCAAGGCGGGCCACGAGCTCGAGCAAATTGGCCAGGACGC
TTGCCATCGATGCTTGCGACTCCGACGTGCGCGCCGCCTTGCTGGACC
TGGACGCGCCAATCGCGGTCTGGCGGCTCCTCGCGCGCCCAAGTCCCG
CCGTGCCCAGTGAGCGCGCTCGGAAGCGCCGCCTTTCGAGCGGCACA
CGGCGTCGATTATGCGCTCTACATGGGCGCAATGGCCAAAGGCGTCG
CGTCAGCGGAGATGGTCATCGCTGCTGGCAAGGCCCGCATGCTCGCGT
CATTTGGCGCGGGGGGGCTTCCCCTGGGCGAGGTCTGAAGAGGCGTTG
GACAAGATCCAGGCCGCTCTGCCCAGGGGGCCGTTCCGCCGTCAACCT
CATTCACTCGCCGTTTCGATCCAAACCITGAGGAGGGCAACGTCGAGCT
GTTCCCTGAGGCGCGGTATCCGGCTGGTCGAGGCCTCTGCGTTCATGTC
GGTCACGCCGTCGTTGGTGCGCTACCGAGTCGCCGGAAGTCGAGCGAG
GCCCTGGCGGGACCGCCCGAGTGCTGAACCGCGTGATTGGCAAGGTG
AGCCGTGCGGAGCTCGCAGAAATGTITATGCGGGCCGCCTCCCGCCGCG
ATCGTCTCCAAGCTCCTCGCCCAGGGCCTGGTCACTGAGGAGCAGGC
GTCACTTGCAAGATCGTCCCCTGGTTGACGACGTTGCAATCGAAGC
CGACTCGGGCGGTACACAGACAACCGCCCGATCCACGTCGTTTTGCC
CGTCGTCTCGCGCTGCGAGACCGCGTCATGCGTGAGTGCAAGTATCC
AGCCGCCAATCGCGTCCGCGTGGGCGCCGGAGGCGGGATCGGCTGCC
CTGCCGCGGCGCGAGCTGCGTTCGACATGGGCGCAGCATTTCGTTCTCA
CGGGCTCGATCAACCAGCTCACGCGCCAGGCTGGGACGAGCGACAGC
GTGCGTGCTGCCCTTGACGCGCGACCTACTCGGACGTGACAATGGCC
CCGGCGGCCGATATGTITGACCAGGGCGTCAAGCTGCAGGTCTTGAAG
CGCGGCACGATGTTCCCGGCGCGCGCAAACAAGCTGTACGAGTTGTT
ACCACTTACCAGTCGCTGGACGCGATCCCTCGGGCTGAGCTGGCTCGC
CTGGAAAAGCGAGTTTTCCGCATGTCCATCGACGAGGTITGGAACGA
AACCAAGCAGTTCTACGAGACCCGGCTCAACAACCCCGCCAAGGTTG
CCCGGGCGGAGCGCGACCCCAAGCTCAAGATGTCGCTCTGCTTTTCGT
GGTACTTGTCGAAAAGCTCCAAGTGGGCATCGACCTGGACAAGTTGGG
CGCGAGCTGGACTACCAGGTCTGGTGCGGCCCCACGATTGGCGCTTTC
AACGAGTTTCGTGAAGGGGTCCAGCCTCGACGCGGAGGCTTGCGGGGG
GCGGTTTTCCTTGCGTTGTGCGCGTTAACCGAGGAGATATTATGTGGCGCT
GCTTACGAGCAGCGACTGGCGCGTTTCATGCTGCTCGCTGGCCGGGAA
AGCGCGGACGCGTTGGCGTACACGGTTGCGGAAGCCAGATAG

SEQ ID NO:10:

RKCIRPSLGHHWAIIGVLGRALRIVRPIRYEATNLRRRLPRSGWLVALGLFCD
LSSCAGKLDLQTRDTAKDPCKRKWSASRAPPRPRAEADKASNEMETKD
DRVAIVGMSAILPCGESVRESWEAIREGLDCLQDLPADRVDITAYYDPNKT
TKDKIYCKRGGFIPEYDFDAREFGLNMFQMEDSDANQTVTLKVKAELED
AGVEPFTKKKKKNIGCVLGIGGGQKASHEFYSLNLYVVVEKVLKMNLPDE
VVEAAVEKYKANFPEWRLDSFPGFLGNVTAGRCSNVFMEGMNCVVDA
ACASSLIAIKVAIDELLHGDCDTMIAGATCTDNSIGMYMAFSKTPVFSTDQ
SVKAYDAKTKGMLIGESAMVVVKRYADAVRDGDEIHAVIRACASSSDGK

FIG.4-10

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AAGIYAPTVSGQEEALRRAYARAGVDPSTVLVEGHGTGTPVGDRIELTAL
RNVFDAANKGRKETVAVGSIKSQIGHLKAVAGFAGLVKVVMMALKHKTLF
QTINVHDPPALHDGSPIQDSSLYINTMNRPWFTAPGVPRRAGISSFGFGGA
NYHAVLEEAPEHAHPYRMNQVPQPVLLHASSASALASICDAQADALQA
AVSPEASKHADYRAIVAFHEAFKLRAGVPAGHARIGFVSGSAAATLAVLR
AASAKLKQSSATLEWTLLREGVTYRSAAMHTPGSVAALFAGQGAQYTHM
FADVAMNWPFFRSVQEMDAAQVTAAAPKRLSEVLYPRKPYAAEPEQD
NKAISMTINSQPALMACAAGAFEVFRQAGLAPDHVAGHSLGFEFGALLAA
GCASREELFRLVCSRAKAMQDVPKPSEGVMAAVIGRGADKLTQGDGAW
LANCNSPSQVVISGDKTAVERESSRLAGLGFRIIPLACEGAFHSPHMTAAQ
ATFQAALDSLKISTPTNGARLYNNVSGKTCRSLGELRDCLGKHMTSPVLFQ
AQVENMYAAGARIFVEFGPKQVLSKLVGEILADKSDFTVAVNSSSSKSDS
VQLREAAAKLAVLGVPLANFDPWELCDARRLRECPRSKTTLRLSAATYVS
NKTAAAREKVMEDNCFSSLFASGPASQEMEREIANLRAELEAAQRQLDT
AKTQLARKQVQDPTADRQRDMIAKHRSTLAAMVKEFEALASGSPCAVPF
APVVDTAVEDVPFADKVSTPPPQVTSAPIAELARAEAVVMEVLAAKTGYE
VDMIEADMMLLDAELGIDSVKRIEILAAVQAQLGVEAKDVDALSRTTRTVGE
VVDAMKAEIGGQATSAPSPMAQPQASAPSPSPTASVLPKPVALPASVDPA
KLARAEAVVMEVLAAKTGYEVDMEADMMLLDAELGIDSVKRIEILAAVQA
QLGVEAKDVDALSRTTRTVGEVVDAMKAEIGGQATSAPASVAQPQASAPS
PSATTASVLPKPVAAPTSADPAKLARAEAVVMEVLAAKTGYEVDMEADM
MLLDAELGIDSVKRIEILAAVQAQLGVEAKDVDALSRTTRTVGEVVEAMKA
EIGGQATSAPASVAQPQISVSPTPLAASPSADPAKLARAEAVVMEVLAAKT
GYEVDMEADMMLLDAELGIDSVKRIEILAAVQAQLGVEAKDVDALSRTTR
VGEVVDAMKAEIGGQATSAPASVAQPQASAPSPSATASVLPKPVAAPTS
DPAKLARAEAVVMEVLAAKTGYEVDMEADMMLLDAELGIDSVKRIEILAA
VQAQLGVEAKDVDALSRTTRTVGEVVEAMKAEIGGQATSAPASMAQPSQIS
VSPTPLAASPSADPAKLARAEAVVMEVLAAKTGYEVDMEADMMLLDAEL
GIDSVKRIEILAAVQAQLGVEAKDVDALSRTTRTVGEVVDAMKAEIGGQAT
SAPASVAQPQASAPSPSATASAPVTPLAAPASVDPAPKLARAEAVVMEVLA
AKTGYEVDMEADMMLLDAELGIDSVKRIEILAAVQAQLGVEAKDVDALS
TRTVGEVVDAMKAEIGGQATSAPASVAQPQASAPSPSATASVLPKPVAS
ASVDPAPKLARAEAVVMEVLAAKTGYEVDMEADMMLLDAELGIDSVKRIE
LAAVQAQLGVEAKDVDALSRTTRTVGEVVEAMKAEIGAAGPNDAQAASG
HLFGTGCEDLSLCSASVVELARCEALERPMDRPILIVSDGSALPAALASRL
GSCAVILTTAGETDQSVRSTKHVDMEGWGEADLVRALEAVESRFGVPGGV
VVLERASETARDQLGFALLAKHSSKALNQIPGGRACFVGVSRIIDGKLGL
SGACAKGKGWAEAAEIAQQGAVAGLCKTLDLEWPHVFARSIDIELGANE
ETAAQAIFEELSCPDLTVREAGYTKDGKRWTTTEARPVGLGKPKQALRSSDV
FLVSGGARGITPVCVRELAKSISGGTFVLLGRSPLADDPAWACGVEEANIG
TAAMAHKAEFAAGRGPKPTPKAHKALVGSVLGAREVLGSLESIRAQGA
RAEYVSCDVSCAERVKAVVDDLERRVGAVTGVVHASGVLRDKSVERLELA
DFEVVYGTKVDGLLNLLQAVDRPKLRHLVLFSSLAGFHGNTGQAVYAMA
NEALNKMAFHLETAMPGLSVKTIGFGPWDGGMVNDALKAHFASMGVQI
IPLDGGGAETVSRIGACSPQTQVLVGNWGLPPVVPNASVHKITVRLGGESAN

FIG.4-11

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PFLSSHTIQGRKVLPMPTVALGLLAEAARGLYVGHQVVGIEDAQVFQGGVVL
DKGATCEVQLRRESSTASPSEVVLSASLNVFAAGKVVPAYRAHVVLGASG
PRTGGVQLELKDLDGVDADPACSVGKGALYDGRTLFHGPAFQYMDEVLR
SPAELAVRCRVVPSAAQDRGQFVSRGVLYDPFLNDTVFQALLVWARLVRD
SASLPSNVERISFHGQPPSEGEVFTTLKLDASAASGPLDPIAKAQFFLHRAC
GAVFASGRASVVLNKALS

SEQ ID NO:11:

QAIGHRAARWSCRKSKARGHKAQKEMNQGGRNDEGVSVARADPCPDT
RIAVVGMAVEYAGCRGKEAFWDTLMNGKINSACISDDRLGSARREEHYA
PERSKYADTFCNERYGCIDPKVDNEHDLGLAAAAALQDAQDRRSDGGK
FDPAQLKRCGIVSGCLSPMDNLQGELNLQYQAHAEERRIGHKCFADQTPW
STRTRALHPLPGDPRTHRDPASFVAGQLGLGPLHYSLEDAACASALYVLR
AQDHLLSGEADMLCGATCFPEPFILTFGSTFHAMPVGENGVSMPPFHRD
TQGLTPGEGGSVMVLKRLADAERDGDHIYGTLLGASLSNAGCGLPLKHQ
PSEEACLKATYELVGVPDRDVQYVECHATGTPQGDVELQAVKACFEGAS
PRIGSTKGNFGHTLVAAGFAGMCKVLLAMERGVIPPTPGVDSGTQIDPLV
VTAALPWPDPTRGGPKRAGLSAFGF GGTNAHAVFEEHIPSRAPPVLCQPR
LGSGPNRKLAIVGMDATFGSLKGLSALEAALYERHAARPLPAKRWRFLG
GDESFLHEIGLECSPHGCYIEDVDVDFKRLRTPMVPEDLLRPQQLLAVSTID
KAILDSGLAKGGNAVVLVGLGTDLELYRHRARVALKERLQGLVRS AEGG
ALTSRLMNYINDSGTSTSYTSYIGNLVATRVSQWGFTGPSFTVTEGANSVH
RCAQLAKYMLDRGEVDAVVVAGVDLCGSAAEFFVRSRRMQISKSQRPA
PFDRAADGFFAGEGCGALVFKRLTDCVSGERIYASLDSVVVATTTPRAALRA
AAGSARVDPASIDMVELSADSHRFVRAPGTVAQPLTAEVEVGAVREVIGT
AGRGSRSVAVGSVRANVG DAGFASGAAALVK TALCLHNRYLAATPGWD
APAAGVDFGAELYVCRESRAWVK NAGVARHAAISGVDEGGSCYGLVLS
VPGQYETGNRISLQAESP KLLLLSAPDHAALLDKVAAELAALEQADGLSA
AAAAVDRLLGESLVGCAAGSGGLTLCLVASPASLHKELALAHRGIPRCIK
ARRDWASPAGSYFAPEPIASDRVAFMYGEGRSPYCGVGRDLHRIWPALHE
RVNAKTVNLWGDGDWLLPRATS AEEEEQLCRNFDSNQVEMFRTGVYIS
MCLTDLARSLIGLGP KASFGLSLGEVSMLFALS ESNCR LSEEMTRRLRASPV
WNS ELAVEFNALRKLWGVAPGAPVDSFWQGYVVRATRAQVEQAIGEDN
QFVRL LIVNDSQSVLIAGKPAACEAVIARIGSILPPLQVSQGMVGHCAEVLP
YTSEIGRIHNMLRFPSQDETGGCKMYSSVSNSRIGPVEESQMGPGTELVFSPS
MEDFVAQLYSRVADFP AITEAVYQQGHDFVEVGPDHSRSAAVRSTLGPT
RRHIAVAMDRKGESAWSQLLKMLATLASHRVPGLDLSSMYHPAVVERCR
LALAAQRSGQPEQRNKFLRTIEVNGFYDPADATIPEAVATILPATAAISPPK
LGAPHDSQPEAEARPVGEASVPRRATSSSKLARTLAIDACDSDVRAALLDL
DAPIAVGGSSRAQVPPCPVSALGSAAFR AAHGV DYALYMGAMAKGVASA
EMVIAAGKARMLASFGAGGLPLGEVEEALDKIQAALPEGPFAVNLIHSPFD
PNLEEGNVELFLRRGIRLVEASAFMSVTPSLVRYRVAGLERGPGGTARVLN
RVIGKVSRAELAEMFMRPPPAIVSKLLAQGLVTEEQASLAEIVPLVDDVAI
EADSGGHTDNRPIHVVLPVVLALRDRVMRECKYPAANRVRVGAGGGGIGC
PAAARA AFDMGA AFVLTGSINQLTRQAGTSDSVRAALARATYSDVTMAP

FIG.4-12

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AADMFDQGVKLQVLKRGTMFPARANKLYELFTTYQSLDAIPRAELARLEK
RVFRMSIDEVWNETKQFYETRLNNPAKVARAERDPKLKMSLCFRWYLSKS
SKWASTGQVGRELDYQVWCGPTIGAFNEFVKGSSLDAEACGGRFPCVVRV
NQEILCGAAAYEQLARFMLLAGRESADALAYTVAEAR

SEQ ID NO:12:

ATGGAGACAAAGGACGATCGCGTTGCGATCGTGGGCATGTCGGCCAT
ACTGCCTTGCGGTGAGTCAGTGC GCGAGTCGTGGGAGGCGATTTCGCG
AGGGGCTCGATTGCCTGCAGGACCTGCCTGCGGACCGAGTCGATATC
ACGGCGTACTACGACCCGAACAAGACAACCAAGGACAAGATCTACT
GCAAGCGCGGCGGCTTCATTCCCGAGTATGACTTTGACGCGCGCGAGT
TCGGCCTCAACATGTTCCAGATGGAGGACTCGGACGCCAACCAAACC
GTGACTTTGCTCAAGGTCAAGGAGGCTCTCGAGGACGCCGGGGTGGA
GCCCTTCACAAAGAAGAAGAAGAACATTGGCTGCGTGCTCGGCATCG
GCGGCGGGCAGAAGGCGAGCCACGAGTTTTACTCCCGACTCAACTAT
GTGGTCGTGGAGAAGGTGCTTCGCAAGATGAACCTCCCCGACGAGGT
TGTCGAGGCCGCGCTCGAAAAGTACAAGGCCAACTTTCCTGAATGGC
GCCTCGACTCGTTCCCTGGGTTTCTTGGAACGTGACCGCCGGGCGGT
GCAGCAACGTCTTCAACATGGAAGGCATGAACTGCGTCGTGGACGCT
GCGTGCGCCAGCTCGCTCATCGCGATCAAGGTTGCCATTGATGAGCTC
CTCCACGGGGACTGCGACACCATGATTGCCGGTGCGACCTGCACCGA
CAACTCGATCGGGATGTACATGGCCTTTTCCAAAACCCAGTTTTCTCC
ACCGACCAGAGCGTCAAGGCGTACGACGCCAAGACGAAAGGCATGC
TCATCGGCGAAGGCTCGGCCATGGTCGTGCTCAAGCGGTACGCGGAC
GCCGTTCTGGGATGGTGATGAGATCCATGCCGTCATCAGGGCATGCGCC
TCGTCCAGCGACGGCAAGGCTGCTGGCATTACGACCGACGGTGTCG
GGTCAAGAAGAGGCACTGCGGCGCGCGTACGCCCAGCTGGCGTGGA
CCCCTCCACCGTCACGCTGGTGAGGGGCCACGGCACTGGCACACCCG
TCGGGGACCGGATTGAGCTGACCGCCTTGCGCAACGTCTTTGACGCAG
CCAACAAAGGCCGCAAGGAAACAGTCGCGGTGGGAAGCATCAAGTC
GCAGATCGGTACCTGAAGGCCGTGGCCGGCTTTGCCGGTCTCGTCAA
GGTTGTCATGGCCCTCAAGCACAAGACGCTGCCGCAGACCATCAACG
TTCACGACCCGCCCGCACTGCACGACGGCTCGCCCATCCAGGATTCGA
GTCTTTACATCAACACGATGAACCGGCCCTGGTTTACGGCACCTGGCG
TCCCCCGCCGTGCAGGCATCTCTAGCTTTGGGTTTGGCGGCGCCAACT
ACCACGCTGTTCTCGAAGAGGCCGAGCCTGAGCACGCGAAGCCGTAT
CGCATGAACCAAGTTCCACAACCGGTGCTCTTGACGCAAGCTCCGCG
TCAGCTCTT

SEQ ID NO:13:

METKDDRVAIVGMSAILPCGESVRESWEAIREGLDCLQDLPADRVDITAYY
DPNRGGFIPEYDFDAREFGLNMFQMEDSDANQTVTLLKVKEALEDAGVEP
FTK
KKKNIGCVLGIGGGQKASHEFY SRLNYVVVEKVLRKMNLPDEVVEAAVEK
YKANFP EWRLDSFPGFLGNV TAGRCSNVFN

FIG.4-13

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MEGMNCVVDAACASSLIAIK
VAIDELLHGDCDTMIAGATCTDNSIGMYMAFSKTPVFSTDQSVKAYDAKT
KGMLIGEGSAMVVLKRYADAVRDGDEIHAVIRACASSSDGKAAGIYAPTV
SGQEEALRRAYARAGVDPSTVTLVEGHGTGTPVGDRIELTALRNVFDAAN
KGRKETVAVG SIKSQIGHLK
AVAGFAGLVKVVMALKHKTLPQTINVHDPP
ALHDGSPIQDSSLYINTMNRPWFTAPGVPRRAGISSFGFGGANYHAVLEE
AEPEHAKPYRMNQVPQPVLLHASSASAL

SEQ ID NO:14:

CAGTCGAGTGCGACGCTCGAATGGACCCTGCTCCGCGAGGGCGTCAC
GTACCGCTCCGCCGCGATGCACACTCCTGGCAGTGTGCTGCTCTGTTT
GCCGGGCAAGGCGCGCAGTACACGCACATGTTCGCTGACGTTGCCAT
GAACTGGCCACCGTTTCGAAGCGCCGTGCAAGAGATGGATGCCGCTC
AAGTCACGGCGGCAGCGCCGAAGCGCCTCAGCGAGGTCCTGTATCCG
CGCAAGCCGTACGCTGCAGAGCCCGAGCAAGACAACAAGGCCATCTC
GATGACGATTAACCTCGCAACCGGCCCTCATGGCCTGCGCTGCTGGGGC
GTTTGAGGTGTTTCGTCAAGCTGGTCTTGCGCCCGACCACGTCGCGGG
TCATTCTCTCGGCGAGTTTGGTGCTTTGCTCGCCGCTGGATGCGCAAGC
CGTGAGGAGCTCTTCCGTCTGGTCTGCAGCAGAGCGAAGGCAATGCA
AGACGTTCCCAAGCCAAGCGAGGGCGTCATGGCAGCTGTCATCGGCC
GTGGTGCTGACAAGCTCACGCTGCAAGGCGATGGTGCGTGGCTTGCCA
ACTGCAACTCGCCAAGCCAAGTGGTCATTTCCGGCGACAAGACTGCT
GTCGAGCGTGAATCCAGCCGGTTGGCAGGCCTTGGCTTCAGGATCATT
CCGCTTGCGATGCGAAGGCGCCTTCCATTCACCGCACATGACGGCGGCC
CAGGCCACGTTTCAGGCTGCACTGGACAGCCTCAAGATCTCCACCCCG
ACGAACGGGGCGCGCCTGTACAACAACGTTTCCGGAAAGACCTGCCG
ATCCCTGGGTGAACTCCGCGACTGCCTGGGCAAGCACATGACAAGTC
CTGTGCTCTTCCAGGCACAGGTAGAGAACATGTACGCTGCCGGGGCG
CGCATTTTCGTGGAGTTTGGCCCGAAGCAAGTCCTCTCCAAGCTCGTA
GGCGAGATTCTCGCCGACAAGTCAGACTTTGTGACAGTCGCGGTCAAC
TCGTCATCGTCCAAGGACAGCGACGTGCAACTTCGTGAAGCTGCTGCG
AAGCTCGCGGTCTTGGCGTCCCGTTGGCGAACTTTGACCCTTGGGAG
CTCTGCGACGCGCGGCGTCTTCGCGAATGCCCGCGATCCAAGACGAC
GTTGCGCTTGTCTGCAGCGACCTACGTGTGCAACAAGACCCTTGCTGC
TAGGGAGAAGGTCATGGAGGACAACTGCGACTTTTCTTCGCTCTTTGC
CTCCGGTCCAGCAAGCCAAGAGATGGAGCGAGAAATAGCCAACCTTC
GCGCTGAGCTGGAGGCGGCCCAACGCCAGCTTGACACGGCCAAA

SEQ ID NO:15:

QSSATLEWTLREGVTYRSAAMHTPGSVAALFAGQGAQYTHMFADVAM
NWPPFRSAVQEMDAAQVTAAPKRLSEVLVPRKPYAAEPEQDNKAISMTI
NSQPALMACAAGAFEVFRQAGLAPDHVAGHSLGEFGALLAAGCASREEL
FRLVCSRAKAMQDVPKPSEGVMAAVIGRGADKLTQGDGAWLANCNSP
SQVVISGDKTAVERESSRLAGLGFRIIPLACEGAFHSPHMTAAQATFQAAL

FIG.4-14

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DSLKISTPTNGARLYNNVSGKTCRSLGELRDCLGKHMTSPVLFQAQVENM
YAAGARIFVEFGPKQVLSKLVGEILADKSDFTVAVNSSSSKDSQVQLREA
AAKLAVLGVPLANFDPWELCDARRLRECPRSKTTLRLSAATYVSNKTLAA
REKVMEDNCDFFSLFASGPASQEMEREIANLRAELEAAQRQLDTAK

SEQ ID NO:16:

CAAGTCACTTCCGCTCCCATCGCCGAGCTCGCGCGCGCCGAGGCCGTC
GTCATGGAGGTTCTCGCTGCCAAGACTGGCTACGAGGTCGACATGATC
GAGGCCGACATGCTGCTCGACGCCGAGCTCGGCATCGACTCGGTCAA
GCGCATTGAGATCCTGGCAGCTGTCCAGGCCAGCTCGGGGTCGAGG
CCAAGGACGTCGACGCGCTCAGCCGCACACGAACAGTTGGCGAGGTC
GTTGACGCCATGAAGGCTGAGATCGGCGGG

SEQ ID NO:17:

QVTSAPIAELARAEAVVMEVLAAKTGYEVDMEADMLLDAELGIDSVKRIE
ILAAVQAQLGVEAKDVDALSRTTVGEVVDAMKAEIGG

SEQ ID NO:18:

CATCTCTTTGGCACGGGATGTGAAGACCTGAGCCTTTGCTCTGCTTCTG
TGGTTGAGATTGCTCGTTGCAGCGAACTAGCTCTGGAGCGCCCGATGG
ATCGGCCCATTTCTTATTGTAAGCGATGGATCAGCATTGCCGGCGGGCTC
TGGCTAGTCGACTGGGGTCGTGTGCAGTAATCCTCACGACCGCAGGGC
AGACCGACCAATCTGTGCGCTCGACGAAGCACGTTGACATGGAAGGG
TGGGGCGAGGCAGATCTCGTGCGCGCTCTTGAAGCAGTAGAGTCTCG
ATTCGGCGTCCCAGGCGGCGTCTGTTGAGCGCGCCTCAGAAAC
AGCTAGGGACCAGCTTGGCTTTGCCCTGCTGCTTGCCAAGCATTGAG
CAAAGCGCTCAACCAGCAGATCCCAGGCGGGCGCGCCTGCTTCGTGG
GCGTCTCGCGAATCGACGGAAAGCTCGGACTTAGCGGAGCTTGCGCG
AAAGGAAAGGGCTGGGCTGAGGCCGCAGAGATTGCTCAGCAAGGAG
CCGTGCGGGGCTTGTGCAAGACCTTGACCTAGAGTGGCCGCACGTCT
TCGCTCGCAGCATCGACATCGAGCTTGGCGCGAACGAAGAAACAGCT
GCGCAAGCAATCTTTGAGGAGCTCTCTTGCCCGGACCTAACGGTGCGC
GAAGCAGGATACACCAAAGACGGCAAGCGGTGGACGACTGAGGCGC
GACCGGTTGGGCTTGGCAAGCCCAAGCAGGCACTACGTTCTTCGGAC
GTCTTCTTGGTTTCTGGTGGGGCGCGGGGAATTACACCTGTTTGCGTTC
GCGAGTTGGCCAAATCGATCAGTGGTGGCACTTTTGTCTCTCTCGGGC
GGTCCCCTCTCGCTGATGATCCGGCGTGGGCTTGCGGGCGTCGAGGAAG
CAAACATTGGGACAGCCGCTATGGCGCACCTCAAGGCCGAGTTCGCA
GCCGGGCGCGGCCCGAAGCCGACGCCAAAGGCCACAAAGCACTCG
TTGGGAGCGTCCTGGGGGCGCGCGAAGTCCTTGGTTTCGCTAGAGAGTA
TTCGCGCCCAGGGTGGCGCGCGCCGAGTACGTTTCTGCGACGTTTCGT
GTGCGGAGCGCGTCAAGGCCGTCGTCGACGATCTCGAGCGACGGGTC
GGGGCTGTAAGTGGGGTTGTGCACGCCTCTGGTGTCTCCGAGACAAG
TCCGTTGAGCGCTTGGAGCTCGCCGACTTCGAGGTCGTGTACGGCACC
AAGGTGGACGGCCTGCTCAACCTGCTGCAGGCCGTGGACCGCCCCAA

FIG.4-15

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ACTCCGGCACTTGGTCCTCTTCAGCTCCCTGGCCGGTTTCCACGGCAAC
ACTGGGCAGGCCGTGTACGCTATGGCGAATGAGGCGCTGAACAAGAT
GGCCTTCCATTTGGAACTGCGATGCCTGGCCTCTCGGTCAAGACGAT
CGGGTTTGGACCTTGGGACGGCGGCATGGTCAACGATGCGCTGAAAG
CGCACTTTGCGTCTATGGGCGTCCAAATTATTCCGCTCGACGGCGGCG
CGGAGACCGTTTCCCGAATCATCGGGGCGTGCTCGCCAACACAAGTTC
TGGTTGGCAACTGGGGCTTGCCCCCTGTAGTTCCTAACGCGAGCGTGC
ACAAGATTACTGTGAGGCTTGGCGGGGAGTCTGCAAACCCTTTCCTGT
CCTCGCACACGATTCAAGGCAGAAAGGTCTTGCCGATGACTGTGGCG
CTTGGGCTTCTCGCTGAGGCGGCTCGAGGGCTCTACGTCGGTCACCAA
GTAGTCGGGATTGAGGACGCCCAAGTCTTCCAGGGAGTCGTGTTGGAC
AAAGGGGCGACGTGTGAGGTCCAGCCGCCGCGAGTCTTCGACTGC
AAGCCCAAGCGAGGTTGTGCTGAGTGCTTCGCTCAATGTATTGCGGCG
GGGAAAGGTTGTGCCTGCGTACCGCGCGCATGTCGTGCTCGGCGCTTC
AGGGCCACGCACTGGCGGCGTGACGCTTGAAGTGAAGATTTGGGCG
TGGACGCCGACCCTGCTTGCTCCGTTGGCAAGGGTGCGCTGTACGACG
GTAGGACGCTGTTCCATGGGCCGCGCTTTCAGTACATGGATGAGGTTC
TTCGGTGCTCGCCTGCAGAGCTTGCCGTGCGGTGCCGTGTCGTTCCGA
GCGCGGCTCAGGACCGCGGCCAATTTGTTTCGCGCGGAGTGTTGTACG
ACCCGTTTCTGAACGACACGGTGTTTCAAGCTCTCCTTGTGTTGGGCCG
TCTGGTCAGGGACAGCGCTTCGCTACCGAGCAACGTTGAACGAATCTC
GTTCCACGGCCAGCCGCCGAGCGAGGGCGAGGTGTTTTACACCACGC
TCAAGCTGGACAGTGCTGCGAGCGGGCCGCTCGACCCGATTGCAAAG
GCGCAGTTCTTCTCCACCGAGCTTGCGGGGCGGTCTTTGCATCAGGG
CGAGCGAGTGTTGTTCTGAACAAGGCTCTTTCGTTT

SEQ ID NO:19:

ASGHLFGTGCEDLSLCSASVVEIARCSELALERPMDRPILIVSDGSALPAAL
ASRLGSCAVILTTAGETDQSVRSTKHVDMEGWGEADLVRALEAVESRFGV
PGGVVVLERASETARDQLGFALLAKHSSKALNQQIPGGRACFVGVSRIDG
KLGLSGACAKKGWAEAAEIAQQGAVAGLCKTLDLEWPHVFARSIDIEL
GANEETAA
QAIFEELSCPDLTVREAGYTKDGKRWTTEARPVGLGKPKQALRSSDVFLV
SGGARGITPVCVRELAKSISGGTFVLLGRSPLADDPACWACGVVEANIGTA
AMAHLKAFAAGRGPKPTPKAHKALVGSVLGAREVLGSLESIRAQGARA
E
YVSCDVSCAERVKAVVDDLERRVGAVTGVVHASGVLRDKSVERLELADFE
VVYGTKVDGLLNLLQAVDRPKLRHLVLFSSLAGFHGNTGQAVYAMANE
AL
NKMAFHLETAMPGLSVKTIGFGPWDGGMVNDALKAHFASMGVQIPLDG
G
AETVSRTIGACSPTQVLVGNWGLPPVVPNASVHKITVRLGGESANPFLSS
HTIQGRKVLPMVALGLLAEAAAGLYVGHQVVGIEDAQVFQGVVLDKGA
T
CEVQLRRESSTASPSEVVLSASLNVFAAGKVVPAYRAHVVLGASGPRTGG

FIG.4-16

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VQLELKDLGVDADPACSVGKGALYDGRTLFGPAFQYMDEVLRCSPAEL
A
VRCRVVPSAAQDRGQFVSRGVLYDPFLNDTVFQALLVWARLVRDSASLPS
NVERISFHGQPPSEGEVIFYTTCLKLDSAASCPLDPIAKAQFFLHRACGAVF
ASGRASVVLNKALSF

SEQ ID NO:20:

ATGAACCAGGGCGGGAGAAATGACGAGGGCGTCTCGGTGGCGCGCGCG
GACCCATGCCCTGACACGCGGATCGCTGTCGTGGGCATCGCGGTTCGAGTA
TGCAGGGTGCCGCGGCAAGGAAGCGTTCTGGGACACGCTCATGAACGGC
AAAATCAACTCTGCCTGTATCTCAGACGATCGCCTCGGGTCAGCACGACG
AGAAGAGCACTATGCGCCCGAGAGGTCAAAGTACGCCGATACGTTCTGC
AACGAGAGGTACGGATGCATCGATCCCAAAGTCGACAACGAGCACGAC
CTGCTCCTCGGCCTCGCCGCGGCTGCGCTTCAAGACGCGCAGGACAGGCG
CAGCGACGGCGGCAAGTTCGACCCAGCGCAGCTCAAGCGCTGCGGCATT
GTCAGCGGCTGCCTGTCCTTCCCGATGGACAACCTGCAAGGCGAGCTGCT
CAACCTTTACCAAGCCCATGCTGAGAGGCGGATTGGCAAGCATTGCTTCG
CGGACCAAACGCCCTGGTCGACGCGAACCAGAGCGCTTCACCCGCTGCC
CGGGGACCCGAGGACCCACCGCGACCCAGCCTCCTTCGTGCGCCGGACAG
CTCGGCCTCGGCCCGCTGCACTACTCGCTCGACGCCGCTGCGCCTCGGC
CCTTTACGTTCTGCGACTCGCTCAGGACCACCTCCTCTCGGGCGAGGCTG
ACTTGATGCTGTGCGGAGCGACGTGCTTCCCAGAGCCCTTCTTCATCCTGA
CTGGGTTTAGCACGTTCCACGCGATGCCAGTCGGTGAGAACGGTGTCTCG
ATGCCGTTTCATCGGGACACGCAAGGGCTGACGCCCGGCGAGGGCGGCT
CGGTGATGGTGCTCAAGCGCCTCGCGGACGCCGAGCGCGACGGAGACCA
CATCTACGGGACGCTTCTTGAGGCCAGCTTGAGCAACGCAGGCTGCGGG
CTTCTCTCAAGCCGCACCAGCCAAGCGAGGAGGCCTGCTTGAAAGCCA
CCTACGAGCTCGTCGGCGTGCCGCCCCGAGACGTCCAGTACGTCGAGTGC
CACGCCACCGGCACGCCGACGGGCGACACCGTCGAGCTCCAAGCCGTCA
AAGCCTGCTTTGAGGGCGCAAGCCCCCGGATCGGGTCCACGAAAGGCAA
CTTCGGACACACCCTCGTCGCGGCCGGCTTTGCGGGAATGTGCAAGGTTT
TCCTTGCAATGGAGCGCGGCGTGATCCCCCGACCCCGGGCGTTGACTCT
GGCACCCAGATTGATCCCCTCGTCGTCACAGCGGCGCTCCCGTGGCCGGA
TACGCGCGGGCGGGCCGAAACGCGCAGGACTCTCCGCATTTCGGATTTCGGG
GGCACAAACGCGCACGCCGTCTTTGAGGAGCATATTCCCTCGAGAGCT

SEQ ID NO:21:

MNQGGRNDEGVSVARADPCPDTRIAVVGMAVEYAGCRGKEAFWDTLMNG
KINSACISDDRLGSARREEHYAPERSKYADTFCNERYGCIDPKVDNEHDLLG
LAAAALQDAQDRSDGGKFDPAQLKRCGIVSGCLSFPMDNLQGELLNLYQA
HAERRIGKHCFADQTPWSTRTRALHPLPGDPRTHRDPASFVAGQLGLGPLHY
SLDAACASALYVLRLAQDHLLSGEADLMLCGATCFPEPFILTFSTFHAMPV
GENGVSMFHRDTQGLTPGEGGSVMVLKRLADAERDGDHIYGTLLGASLSN
AGCGLPLKPHQPSEEACLKATYELVGVPFRDVQYVECHATGTTPQGDVELQA
VKACFEGASPRIGSTKGNFGHTLVAAGFAGMCKVLLAMERGVIPPTPGVDSG

FIG.4-17

TQIDPLVVTAALPWPDTTRGGPKRAGLSAFGFGGTNAHAVFEEHIPSRA

SEQ ID NO: 22:

CAGCCTCGCCTCGGCAGCGGACCAAACCGAAAGCTTGCTATCGTCGGCA
TGGATGCCACGTTTGGATCCTTGAAGGGTCTCTCCGCACTAGAAGCTGCG
CTTTACGAGGCAAGGCACGCTGCGCGGCCCCCTGCCTGCGAAGCGCTGGC
GCTTCTTGGGCGGGGACGAGTCCTTTCTCCACGAGATCGGACTCGAGTGC
TCTCCGCACGGGTGCTACATTGAGGACGTGGATGTGGACTTTAAGCGACT
CCGCACGCCAATGGTGCCGGAGGACTTGCTCCGGCCGCAACAGCTCCTG
GCCGTGTCGACGATTGACAAGGCCATCCTCGACTCGGGCTTGGCCAAGG
GCGGCAACGTGGCTGTCTTGTGCGCCTCGGGACGGACCTCGAGCTCTAC
CGCCACCGAGCTCGGGTTGCGCTTAAGGAGCGTCTTCAAGGACTGGTTCG
CTCTGCCGAGGGAGGAGCCCTGACGTCTCGCCTGATGAACTATATCAATG
ATAGCGGAACGTGACCTCCTACACGTTCGTATATCGGCAACCTCGTCGCC
ACGCGCGTCTCGTCCCAGTGGGGCTTCACTGGGCGCGTCGTTACCGTCAC
GGAAGGGGGCCAACTCGGTCCATCGGTGCGCCCAGCTCGCCAAGTACATG
CTCGACCGCGGCGAGGTGACGCGCGTCGTGGTTGCAGGAGTCGACCTGTG
CGGGAGCGCCGAGGCGTTCTTCGTGAGGTGCGCGCCGCATGCAGATCTCGA
AAAGTCAGCGCCCGGCCGCGCCGTTTGACCGCGCCGCAGACGGCTTCTTC
GCGGGGGAAGGGTGCGGCGCCCTCGTCTTCAAACGCCTGACTGACTGTGT
GTCTGGCGAGCGAATCTACGCGTCCCTCGACTCGGTGCTCGTCGCAACCA
CGCCGCGCGCCGCTCTTCGTGCTGCCGCAGGGTCGGCGCGGGTTGACCCA
GCCAGCATCGACATGGTCGAGCTGAGCGCAGATTCCCACCGGTTTGTGCG
GGCGCCAGGCACCGTGGCTCAGCCTCTGACAGCCGAAGTCGAGGTGCGG
GCGGTGCGGGAAGTGATCGGGACCGCGGGGAGGGGCTCTCGAAGCGTGG
CCGTGCGATCGGTCCGCGCCAACGTGCGGGACGCAGGGTTTGCTTCCGGG
GCCGCTGCCCTCGTAAAACTGCGCTCTGCTTGACACAACCGCTACTTGGC
GGCTACCCAGGCTGGGATGCGCCTGCTGCCGGCGTGGATTTTGGTGCCG
AGCTGTACGTTTGCCGCGAGTCGCGTGCTTGGGTCAAGAACGCCGGCGTT
GCACGGCACGCCGCAATTTCTGGCGTGGACGAAGGCGGGTCG

SEQ ID NO:23:

QPRLGSGPNRKLAIVGMDATFGSLKGLSALEAALYEARHAARPLPAKRWRFL
GGDESFLHEIGLECSPHGCIYEDVDVDFKRLRTPMPEDLLRPQQLLAVSTIDK
AILDGLAKGGNVAVLVGLGTDLELYRHRARVALKERLQGLVRSAGGALTS
RLMNYINDSGTSTSYTSYIGNLVATRVSQWGFTGPSFTVTEGANSVHRCAQL
AKYMLDRGEVDVAVVAGVDLCGSAEFFVRSRRMQISKSQRPAAPFDRAAD
GFFAGEGCGALVFKRLTDCVSGERIYASLDSVVVATTPRAALRAAAGSARVDP
ASIDMVELSADSHRFVRAPGTVAQPLTAEVEVGAVREVIGTAGRGSRVAVGS
VRANVG DAGFASGAAALVK TALCLHNRYLAATPGWDAPAAGVDFGAELYV
CRESRAWVK NAGVARHAAISGVDEGGS

SEQ ID NO:24:

TGCTATGGGCTGGTTCTTTTCGGACGTGCCTGGCAGTACGAGACCGGCAA

FIG.4-18

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CCGCATCTCCCTCCAGGCCGAGTCGCCCAAGCTCTTGCTCCTCTCGGTCC
AGACCACGCCGCCTTGCTGGACAAGGTGGCGGCCGAGCTCGCAGCCCTT
GAGCAAGCCGACGGCTTGAGCGCCGCCGCGGCTGCCGTAGACCGCTTAC
TCGGCGAGTCGCTCGTCGGTTGCGCGGCTGGCAGCGGGCGGGCTGACCCTT
TGCTTGGTGGCTTCGCCTGCCAGCCTCCACAAGGAGCTTGCGCTGGCCCA
TCGAGGGATCCCGCGCTGCATCAAAGCACGGCGCGACTGGGCCAGCCCCG
GCAGGGAGCTACTTCGCCCCGGAGCCGATCGCAAGCGACCGCGTCGCGT
TCATGTACGGGGAAGGACGAAGCCCGTACTGCGGCGTCGGCCGCGACCT
CCACCGGATCTGGCCCCGCGCTGCATGAGCGGGTGAACGCCAAGACTGTC
AACCTCTGGGGTGACGGTGACGCCTGGCTGCTGCCACGTGCAACCTCGGC
CGAGGAAGAGGAGCAACTCTGCCGCAACTTCGACTCGAACCAGGTTGAG
ATGTTTCGAACGGGCGTGTACATCTCGATGTGCTTGACCGACCTCGCTCG
AAGCTTGATTGGACTGGGCCCTAAGGCGAGCTTTGGGCTCAGCCTAGGCG
AGGTTTCCATGCTCTTCGCTCTGAGCGAGTCCAACTGTAGACTGTCCGAG
GAAATGACCCGCAGGCTCCGTGCGTCCCCGGTGTGGAACCTCGGAGCTCG
CCGTTCGAGTTCAACGCCCTTCGAAAGTTGTGGGGGGGTGCGCGCCGGGGGC
ACCCGTCGACTCGTTCTGGCAAGGTTATGTCGTGCGCGCAACGCGGGCTC
AGGTGGAGCAAGCCATTGGGGAGGACAATCAGTTTGTGCGTCTCCTGATC
GTGAACGACTCGCAATCAGTCCTGATCGCCGGCAAGCCGGCGGCGTGCG
AAGCCGTAATTGCTCGCATCGGGTCTATTCTTCCCCCGCTGCAAGTGTGCG
AAGGCATGGTGGGGCACTGTGCCGAGGTCTTGCCGTACACGAGCGAGAT
CGGGCGCATCCACAACATGCTTCGCTTCCCATCGCAGGACGAAACGGGC
GGTTGCAAAATGTACTCTAGCGTCTCAAACCTCGCGCATCGGGCCAGTCGA
GGAGAGCCAGATGGGCCCAGGCACTGAGCTCGTTTTCTCGCCGTCAATGG
AAGACTTTGTGCCCCAGCTGTACTCGCGAGTTGCAGACTTTCCGGCGATC
ACCGAGGCGGTTTACCAGCAGGGTTCATGACGTGTTTGTGCAAGTGGGGCC
GGACCATTCACGGTCGGCTGCTGTCCGCTCCACGCTTGGAACCACTCGGC
GACACATCGCTGTGGCGATGGACCGCAAGGGTGAGTCAGCTTGGTCGCA
GCTTCTGAAAATGCTGGCTACGCTTGCGTCGCACCGCGTGCCGGGCCTG

SEQ ID NO:25:

CYGLVLSDPGQYETGNRISLQAESPKLLLLSAPDHAALLDKVAAELA ALEQA
DGLSAAAAAVDRLLGESLVGCAAGSGGLTLCLVASPASLHKELALAHRGIPR
CIKARRDWASPAGSYFAPEPIASDRVAFMYGEGRSPYCGVGRDLHRIWPALHE
RVNAKTVNLWGDGDAWLLPRATSAAAAEQLCRNFDNQNQVEMFRTGVYISM
LTDLARSLIGLGP KASFGLSLGEVSM LFALSESNCR LSEEMTRRLRASPVWNSEL
AVEFNALRKLWGVAPGAPVDSFWQGYVVRATRAQVEQAIGEDNQFVRLLIV
NDSQSVLIAGKPAACEAVIARIGSILPPLQVSQGMVGHCAEVLPTSEIGRIHN
MLRFPSQDETGGCKMYSSVNSNRIGPVEESQMGPTEL VFSPSMEDFVAQLYSR
VADFPAITEAVYQQGHDVFVEVGP DHSRSAAVRSTLGPTRRHIAVAMDRKGE
SAWSQLKMLATLASHRVPGL

SEQ ID NO:26:

GCGACCATCCCTGAGGCCGTCGCAACAATTCTGCCGGCAACTGCTGCGAT
TTCGCCTCCAAAGCTTGGCGCTCCGCACGACTCGCAACCCGAGGCGGAG

FIG.4-19

25/25

GCTCGCCCCGTGGGCGAGGCCTCTGTGCCAAGGCGGGGCCACGAGCTCGA
GCAAATTGGCCAGGACGCTTGCCATCGATGCTTGCGACTCCGACGTGCGC
GCCGCCTTGCTGGACCTGGACGCGCCAATCGCGGTCGGCGGCTCCTCGCG
CGCCCAAGTCCCGCCGTGCCAGTGAGCGCGCTCGGAAGCGCCGCCTTTC
GAGCGGCACACGGCGTCGATTATGCGCTCTACATGGGCGCAATGGCCAA
AGGCGTCGCGTCAGCGGAGATGGTCATCGCTGCTGGCAAGGCCCGCATG
CTCGCGTCATTTGGCGCGGGGGGGCTTCCCCTGGGCGAGGTCGAAGAGGC
GTTGGACAAGATCCAGGCCGCTCTGCCCGAGGGGCGGTTTCGCCGTCAACC
TCATTCACTCGCCGTTTCGATCCAAACCTTGAGGAGGGCAACGTCGAGCTG
TTCCTGAGGCGCGGTATCCGGCTGGTCGAGGCCTCTGCGTTTCATGTCGGTC
ACGCCGTCGTTGGTGCGCTACCGAGTCGCCGGACTIONGAGCGAGGCCTG
GCGGGACCGCCCGAGTGCTGAACCGCGTGATTGGCAAGGTGAGCCGTGC
GGAGCTCGCAGAAATGTTTATGCGGCCGCCTCCCGCCGCGATCGTCTCCA
AGCTCCTCGCCCAGGGCCTGGTCACTGAGGAGCAGGCGTCACTTGCAGA
GATCGTCCCACTGGTTGACGACGTTGCAATCGAAGCCGACTCGGGCGGTC
ACACAGACAACCGCCCGATCCACGTCGTTTTGCCCGTCGTCCTCGCGCTG
CGAGACCGCGTCATGCGTGAGTGCAAGTATCCAGCCGCCAATCGCGTCC
GCGTGGGCGCCGGAGGCGGGATCGGCTGCCCTGCCGCGGCGCGAGCTGC
GTTCGACATGGGCGCAGCATTCGTTCTCACGGGCTCGATCAACCAGCTCA
CGCGCCAGGCTGGGACGAGCGACAGCGTGCGTGCTGCCCTTGCACGCGC
GACCTACTCGGACGTGACAATGGCCCCGGCGGCCGATAGTTTGACCAG
GGCGTCAAGCTGCAGGTCTTGAAGCGCGGCACGATGTTCCCGGCGCGCG
CAAACAAGCTGTACGAGTTGTTTACCACCTACCAGTCGCTGGACGCGATC
CCTCGGGCTGAGCTGGCTCGCCTGGAAAAGCGAGTTTTCCGCATGTCCAT
CGACGAGGTTTGGAAACGAAACCAAGCAGTTCTACGAGACCCGGCTCAAC
AACCCCGCCAAGGTTGCCCGGGCGGAGCGCGACCCCAAGCTCAAGATGT
CGCTCTGCTTTTCGGTGGTACTTGTCGAAAAGCTCCAAGTGGGCATCGACT
GGACAAGTTGGGCGCGAGCTGGACTACCAGGTCTGGTGCGGCCCCACGA
TTGGCGCTTTCAACGAGTTCGTGAAGGGGTCCAGCCTCGACGCGGAGGCT
TGCGGGGGGGCGGTTTTCTTGCGTTGTGCGCGTTAACCAGGAGATATTATG
TGGCGCTGCTTACGAGCAGCGACTGGCGCGTTTTTCATGCTGCTCGCTGGCC
GGGAAAGCGCGGACGCGTTGGCGTACACGGTTGCGGAAGCCAGATAG

SEQ ID NO:27:

ATIEAVATILPATAAISPPKLGAPHDSQPEAEARPVGEASVPRRATSSSKLART
LAIDACDSDVRAALLDLDAPIAVGGSSRAQVPPCPVSALGSAAFRAAHGVDY
ALYMGAMAKGVASAEMVIAAGKARMLASFGAGGLPLGEVEEALDKIQAALP
EGPFAVNLIHSPFDPNLEEGNVELFLRRGIRLVEASAFMSVTPSLVRYRVAGLE
RGPGGTARVLNRVIGKVSRAELAEMFMRPPPAIVSKLLAQGLVTEEQASLAE
IVPLVDDVAIEADSGGHTDNRPIHVVLPLVVLALRDRVMRECKYPAANRVRVG
AGGGIGCPAAARAFAFDMGAFFVLTGSINQLTRQAGTSDSVRAALARATYSDV
TMAPAAMFDQGVKLQVLKRGTMFPARANKLYELFTTYQSLDAIPRAELARL
EKRVFRMSIDEVWNETKQFYETRLNNPAKVARAERDPKLMKMSLCFRWYLSKS
SKWASTGQVGRELDYQVWCGPTIGAFNEFVKGSSLDAAECGGRFPCVVRVN
QEILCGAAEYEQRLARFMLLAGRESADALAYTVAEAR

FIG.4-20